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Genome-Wide Association Study of Fatness in Chickens

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Summary and Implications

A genome-wide association study of fatness was performed using a high-density genotyping platform and two F2 resource populations established by crossing one broiler sire with dams from two unrelated highly inbred lines (Fayoumi and Leghorn). In total, 24 and 30 markers showed a significant association ($P<0.01$) with abdominal fat percentage in Broiler × Fayoumi (B × F) and Broiler × Leghorn (B × L) crosses, respectively. Compared to a previous scan in the same populations, with about one-tenth the marker density, the current study identified 12 additional genomic regions for fatness. These results demonstrate the power of high marker-density association studies in discovering quantitative trait loci (QTL).

Introduction

Excessive fat deposition in meat type chickens has negative impacts on feed efficiency, nitrogen retention and lean meat yield. Although fatness is a highly heritable trait, the difficulty and cost of measuring fat are two major limitations for commercial selection against this trait. Molecular genetics techniques can help to identify the genetic markers for fatness and facilitate the use of marker information in selection programs. To date, the study of quantitative traits in chicken was based on genetic markers which are less frequent than single-nucleotide polymorphism (SNP) markers in genome. The recent availability of the complete genome sequence of the chicken, a polymorphism map and high-density SNP genotyping platforms provide powerful tools for genome-wide association studies of quantitative traits in chicken.

Materials and Methods

The Iowa Growth and Composition Resource Population (IGCRP) was established by crossing broiler sires with dams from two unrelated highly inbred lines. About 720 F2 offspring, all from one broiler grandsire, were produced in three hatches. At eight weeks of age, the birds were euthanized and abdominal fat weight and body weight were recorded.

A high-density genotyping platform (Illumina Bead Array) was used for genotyping about 3000 SNP. In each F2 population, selective genotyping was carried out for 20 extreme (high or low) individuals for abdominal fat weight as a percentage of body weight (AF) at 8 weeks of age. One individual from each inbred line as the representative of these lines and the broiler grandsire were also genotyped. Single-point statistical association analysis was performed by regressing phenotype (AF) on SNP genotype in each F2 population.

Results and Discussion

The results of single point association analysis showed significant association ($P<0.01$) of 24 and 30 markers with AF in B × F and B × L crosses, respectively. These markers were located in 13 chromosomes (GGA1, 2, 3, 4, 7, 8, 10, 11, 12, 15, 24, 27, and Z).

Dominance and cryptic allele patterns were assessed for markers that were homozygous for alternative alleles in the F0 parents. More than 70% of SNP showed cryptic effect. About 40% of SNP showed dominant pattern. There was a two-fold higher proportion of markers with dominant inbred line alleles than dominant broiler line alleles. In B × F cross, two markers showed over-dominance pattern in opposite direction. Markers that were clustered close to each other showed the same dominance and cryptic patterns.

Compared to a previous marker QTL scan in the same populations, with about one-tenth the marker density, the current study identified 12 additional QTL regions for fatness. Besides, the results of the current study provide important information on genetic architecture of fatness. These new findings are helpful in identifying markers close to fatness-controlling genes and in implementation of marker-assisted selection in breeding programs.

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